

STIC-ILL

ND 432161 102

From: Portner, Ginny  
Sent: Thursday, February 13, 2003 2:03 PM  
To: STIC-ILL  
Subject: 09/895,913

Importance: High

00453860 INSIDE CONFERENCE ITEM ID: CN004355891  
Molecular Cloning and Nucleotide Sequence Determination of htrA , a Gene  
Encoding a 48-kDa Stress Protein of Helicobacter pylori  
Kleanthous, H.; Clayton, C. L.; Morgan, D. D.; Pallen, M. J.  
CONFERENCE: Basic and clinical aspects of helicobacter pylori infection-  
4th Workshop  
P: 195-202  
New York, Springer-Verlag, c1994  
ISBN: 3540567208; 0387567208  
LANGUAGE: English DOCUMENT TYPE: Conference Selected papers  
CONFERENCE EDITOR(S): Gasbarrini, G.; Pretolani, S.  
CONFERENCE SPONSOR: European Helicobacter Pylori Study Group  
CONFERENCE LOCATION: Boiogna, Italy  
CONFERENCE DATE: Nov 1991 (199111) (199111)

BRITISH LIBRARY ITEM LOCATION: 94/09285 Basic

NOTE:

xii, 313 p.; Described as proceedings. See also 4588.3404 vol 23 no 9  
and supp 1 2 1991 for abstracts and programme

DESCRIPTORS: helicobacter pylori infection; helicobacter pylori.

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C1577  
2/14

|    |                 |  |     |       |
|----|-----------------|--|-----|-------|
| tr | <u>O25663</u>   | Serine protease (HTRA) [HP1019] [Helicobacter pylori (...] | 834 | 0.0   |
| tr | <u>Q9ZM18</u>   | Protease DO [HTRA] [Helicobacter pylori J99 (Campyloba...  | 813 | 0.0   |
| tr | <u>Q9PN69</u>   | Serine protease (Protease DO) (EC 3.4.21.-) [HTRA] [Ca...  | 388 | e-107 |
| tr | <u>Q46120</u>   | Serine protease [HTRA] [Campylobacter jejuni]              | 387 | e-106 |
| tr | <u>Q46094</u>   | Heat shock protein/serine protease (Fragment) [HTRA] [...] | 347 | 2e-94 |
| tr | <u>Q8YHL4</u>   | Protease DO (EC 3.4.21.-) [BMEI0783] [Brucella meliten...  | 291 | 1e-77 |
| tn | <u>AAN30126</u> | Serine protease [BR1207] [Brucella suis]                   | 291 | 1e-77 |
| tr | <u>Q44596</u>   | HtrA-like protein [Brucella abortus]                       | 289 | 4e-77 |
| sp | <u>P18584</u>   | DEGP_CHLTR Probable serine protease do-like precursor ...  | 289 | 5e-77 |
| tr | <u>Q9FD11</u>   | HtrA-like serine protease [PRTS1] [Aeromonas hydrophila]   | 288 | 7e-77 |
| tn | <u>AAN56917</u> | Serine protease, HtrA/DegQ/DegS family [SO3942] [She...    | 287 | 2e-76 |
| tr | <u>Q9KUF5</u>   | Protease DO [VC0566] [Vibrio cholerae]                     | 286 | 3e-76 |
| tr | <u>Q8XV99</u>   | Probable HTRA-like serine protease signal peptide prot...  | 286 | 3e-76 |
| tn | <u>AAO09118</u> | Protease DO [VV10603] [Vibrio vulnificus]                  | 286 | 3e-76 |
| sp | <u>Q9PL97</u>   | DEGP_CHLMU Probable serine protease do-like precursor ...  | 285 | 6e-76 |
| tr | <u>Q8KCH4</u>   | Serine protease [CT1447] [Chlorobium tepidum]              | 285 | 6e-76 |
| sp | <u>Q9Z6T0</u>   | DEGP_CHLPN Probable serine protease do-like precursor ...  | 282 | 5e-75 |
| tr | <u>Q8L1C3</u>   | DegQ serine protease [Pasteurella piscicida (Photobact...  | 276 | 4e-73 |
| tn | <u>BAC24289</u> | DegQ protein [degQ] [Wigglesworthia brevipalpis]           | 276 | 5e-73 |
| tn | <u>AAN66925</u> | HtrA-like protease AlgW [algW] [Pseudomonas putida]        | 275 | 1e-72 |
| tr | <u>Q57155</u>   | MUCD (Serine protease MUCD) [MUCD] [Pseudomonas aerugi...  | 273 | 2e-72 |
| tr | <u>Q9AL31</u>   | MucD [MUCD] [Pseudomonas aeruginosa]                       | 273 | 2e-72 |
| tr | <u>Q8Z9B0</u>   | Protease DO, heat shock protein HtrA [STY0231] [Salmon...  | 272 | 5e-72 |
| tn | <u>AAN78691</u> | Protease do precursor (EC 3.4.21.-) [htrA] [Escheric...    | 272 | 7e-72 |
| sp | <u>P26982</u>   | DEGP_SALTY Protease do precursor (EC 3.4.21.-) [DEGP] ...  | 271 | 1e-71 |
| tn | <u>BAC50633</u> | Serine protease [bll5368] [Bradyrhizobium japonicum]       | 271 | 2e-71 |
| sp | <u>P09376</u>   | DEGP_ECOLI Protease do precursor (EC 3.4.21.-) [DEGP] ...  | 270 | 2e-71 |
| tn | <u>AAN41816</u> | Periplasmic serine protease Do, heat shock protein H...    | 268 | 1e-70 |
| tr | <u>Q98CS8</u>   | Serine protease, HtrA/DegQ/DegS family [MLL5022] [Rhiz...  | 267 | 2e-70 |
| tr | <u>O67436</u>   | Periplasmic serine protease [HTRA] [Aquifex aeolicus]      | 264 | 1e-69 |
| tr | <u>Q9LBK0</u>   | Heat shock protein HtrA [HTRA] [Shigella sonnei]           | 264 | 1e-69 |
| tr | <u>Q9HVX1</u>   | AlgW protein [ALGW] [Pseudomonas aeruginosa]               | 263 | 2e-69 |
| sp | <u>P45129</u>   | HTOA_HAEIN Probable periplasmic serine protease do/hho...  | 262 | 5e-69 |
| tr | <u>Q8RSS1</u>   | HtrA protein [HTRA] [Klebsiella pneumoniae]                | 262 | 5e-69 |
| tr | <u>Q8ZB58</u>   | Protease (EC 3.4.21.-) [DEGQ] [Yersinia pestis]            | 262 | 7e-69 |
| tn | <u>AAM83731</u> | Serine endoprotease [degQ] [Yersinia pestis]               | 262 | 7e-69 |
| tr | <u>Q9AQD1</u>   | MucD [MUCD] [Pseudomonas syringae (pv. syringae)]          | 260 | 3e-68 |
| tr | <u>Q8UE46</u>   | Serine protease [HTRA] [Agrobacterium tumefaciens (str...  | 259 | 6e-68 |
| tr | <u>Q8UGQ8</u>   | Serine protease DO-like protease [DOP] [Agrobacterium ...] | 258 | 8e-68 |
| tr | <u>O68198</u>   | HtrA [Haemophilus influenzae]                              | 257 | 2e-67 |
| tr | <u>O68197</u>   | HTRA (Fragment) [Haemophilus influenzae]                   | 257 | 2e-67 |
| tr | <u>O31388</u>   | DegP protein [DEGP] [Bradyrhizobium japonicum]             | 256 | 3e-67 |
| tn | <u>BAC50500</u> | Serine protease [degP] [Bradyrhizobium japonicum]          | 256 | 3e-67 |
| sp | <u>Q92JA1</u>   | DEGP_RICCN Probable serine protease do-like precursor ...  | 255 | 7e-67 |
| tn | <u>AAN67052</u> | Alginate biosynthesis negative regulator, serine pro...    | 255 | 7e-67 |
| tr | <u>Q8P418</u>   | Protease Do [HTRA] [Xanthomonas campestris (pv. campes...  | 254 | 1e-66 |
| tr | <u>Q9CMS7</u>   | HtrA [HTRA] [Pasteurella multocida]                        | 254 | 1e-66 |
| tr | <u>P74978</u>   | GsrA protein [GSRA] [Yersinia enterocolitica]              | 254 | 1e-66 |
| sp | <u>P39099</u>   | DEGQ_ECOLI Protease degQ precursor (EC 3.4.21.-) [DEGQ...  | 253 | 2e-66 |
| tr | <u>Q8X9F1</u>   | Serine endoprotease [DEGQ] [Escherichia coli O157:H7]      | 253 | 2e-66 |
| tr | <u>Q8ZBM6</u>   | Global stress requirement protein GsrA [GSRA] [Yersini...  | 253 | 2e-66 |
| tn | <u>AAM84394</u> | Periplasmic serine protease Do [htrA] [Yersinia pestis]    | 253 | 2e-66 |
| tn | <u>AAN82429</u> | Protease degQ precursor (EC 3.4.21.-) [degQ] [Escher...    | 253 | 2e-66 |
| sp | <u>Q44597</u>   | DEGP_BRUAB Probable serine protease do-like precursor ...  | 252 | 6e-66 |
| tr | <u>Q8PFK1</u>   | Protease DO [HTRA] [Xanthomonas axonopodis (pv. citri)]    | 252 | 6e-66 |
| tr | <u>Q8YG32</u>   | Protease DO (EC 3.4.21.-) [BMEI1330] [Brucella meliten...  | 252 | 6e-66 |
| tn | <u>BAC48395</u> | Serine protease DO-like precursor [blr3130] [Bradyrh...    | 252 | 7e-66 |
| sp | <u>P57322</u>   | DEGP_BUCAI Probable serine protease do-like precursor ...  | 251 | 1e-65 |
| tr | <u>Q8UDS7</u>   | Serine protease DO-like [HTRA] [Agrobacterium tumefaci...  | 251 | 1e-65 |
| tn | <u>AAO26942</u> | Serine protease (EC 3.4.21.-) [htrA] [Buchnera aphid...    | 251 | 2e-65 |
| tr | <u>Q8Z3E6</u>   | Serine protease (EC 3.4.21.-) [DEGQ] [Salmonella typhi]    | 248 | 8e-65 |
| tr | <u>Q98N31</u>   | Heat shock protein HtrA like [MLR0328] [Rhizobium loti...  | 247 | 2e-64 |
| tr | <u>Q8ZLQ1</u>   | Serine endoprotease (EC 3.4.21.-) [DEGQ] [Salmonella t...  | 247 | 2e-64 |
| tr | <u>Q9PGL3</u>   | Heat shock protein [XF0285] [Xylella fastidiosa]           | 247 | 2e-64 |
| tr | <u>Q8KKV0</u>   | Hypothetical protein [HTRA] [Rhizobium etli]               | 247 | 2e-64 |

|    |          |   |     |       |
|----|----------|---|-----|-------|
| tn | AAO28122 | Heat shock protein [htrA] [Xylella fastidiosa Temecu...   | 247 | 2e-64 |
| tr | Q8XPT5   | Probable protease signal peptide protein (EC 3.4.-.-) ... | 246 | 5e-64 |
| sp | O85291   | DEGP_BUCAP Probable serine protease do-like precursor ... | 245 | 7e-64 |
| tn | BAC51771 | Serine protease DO-like precursor [bll6506] [Bradyrh...   | 245 | 7e-64 |
| tr | Q985F9   | Serine protease [MLR7692] [Rhizobium loti (Mesorhizobi... | 244 | 2e-63 |
| tr | Q56885   | HtrA protein (Fragment) [HTRA] [Yersinia enterocolitica]  | 244 | 2e-63 |
| tn | BAC47856 | Serine protease DO-like protease [dop] [Bradyrhizobi...   | 244 | 2e-63 |
| tr | Q92QE6   | Probable protease protein (EC 3.4.21.-) [DEGP3] [Rhizo... | 243 | 3e-63 |
| tr | Q44652   | Immunoreactive stress response protein precursor [Bruc... | 240 | 3e-62 |
| tr | Q98KJ1   | Probable serine protease [MLL1451] [Rhizobium loti (Me... | 239 | 5e-62 |
| tr | Q9PBA3   | Periplasmic protease [XF2241] [Xylella fastidiosa]        | 238 | 8e-62 |
| tn | AAO29135 | Periplasmic protease [mucD] [Xylella fastidiosa Teme...   | 237 | 2e-61 |
| tr | Q926C8   | Putative protease precursor signal peptide protein (EC... | 237 | 2e-61 |
| tr | Q8PB56   | Periplasmic protease [MUCD] [Xanthomonas campestris (p... | 234 | 1e-60 |
| tr | Q8PMV4   | Periplasmic protease [MUCD] [Xanthomonas axonopodis (p... | 234 | 1e-60 |
| tr | Q8RTK2   | Protease MucD [MUCD] [Xanthomonas campestris (pv. camp... | 234 | 1e-60 |
| tn | AAN44738 | Serine endoprotease [degQ] [Shigella flexneri]            | 234 | 1e-60 |
| sp | O05942   | DEGP_RICPR Probable serine protease do-like precursor ... | 234 | 2e-60 |
| sp | F54925   | DEGP_BARHE Probable periplasmic serine protease DO-lik... | 233 | 3e-60 |
| sp | Q52894   | DEGP_RHIME Probable serine protease do-like precursor ... | 232 | 6e-60 |
| tr | Q8Y0I6   | Probable periplasmic protease signal peptide protein (... | 231 | 1e-59 |
| tr | F73354   | Serine protease HTRA [HTRA] [Synechocystis sp. (strain... | 231 | 1e-59 |
| tr | Q9JVT1   | Putative periplasmic serine protease (EC 3.4.21.-) [NM... | 230 | 3e-59 |
| tn | AAN48008 | Serine protease DO [LA0809] [Leptospira interrogans]      | 229 | 4e-59 |
| tr | Q8YI32   | Protease DO (EC 3.4.21.-) [BMEI0613] [Brucella meliten... | 228 | 9e-59 |
| tn | AAN30307 | Serine protease Do, putative [BR1394] [Brucella suis]     | 228 | 9e-59 |
| tr | Q9KJN6   | Putative serine protease DO-like [HTRA] [Myxococcus xa... | 225 | 1e-57 |
| tr | Q9A4S2   | Serine protease HtrA [CC2758] [Caulobacter crescentus]    | 223 | 4e-57 |
| tr | O06439   | ORF E0 protein [Rhodobacter capsulatus (Rhodopseudomon... | 222 | 8e-57 |
| tn | BAC08222 | Periplasmic serine proteinase [tlr0671] [Synechococc...   | 219 | 7e-56 |
| tr | Q9WZ41   | Heat shock serine protease, periplasmic [TM0571] [Ther... | 218 | 9e-56 |
| tr | Q51374   | AlgW [Pseudomonas aeruginosa]                             | 218 | 1e-55 |
| tr | Q8YVH0   | Serine proteinase [ALL2008] [Anabaena sp. (strain PCC ... | 215 | 1e-54 |
| sp | P44947   | DEGS_HAEIN Protease degS precursor (EC 3.4.21.-) [DEGS... | 214 | 2e-54 |
| tr | Q9A8R9   | Serine protease [CC1282] [Caulobacter crescentus]         | 209 | 7e-53 |

|                                      |                              |                                   |                            |                                      |                            |
|--------------------------------------|------------------------------|-----------------------------------|----------------------------|--------------------------------------|----------------------------|
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### Welcome to the SIB BLAST Network Service

If results of this search are reported or published, please mention that the computation was performed at the SIB using the BLAST network service. The SIB BLAST network service uses a server developed at SIB and the NCBI BLAST 2 software. It is implemented on hardware provided by HP.

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NCBI BLAST program reference [PMID:9254694]:

Altschul S.F., Madden T.L., Schäffer A.A., Zhang J., Zhang Z., Miller W., Lipman D.J. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25:3389-3402(1997).

Query length: 443 AA (of which 3% low-complexity regions filtered out)  
 Date run: 2003-02-13 14:19:37 UTC+0100 on sib-blast.unil.ch  
 Program: NCBI BLASTP 2.2.5 [Nov-16-2002]  
 Database: XXtremblnew; XXtrembl; XXswissprot  
           1,034,081 sequences; 330,203,360 total letters  
           Swiss-Prot Release 40.43 of 12-Feb-2003  
           TrEMBL Release 22.12 of 07-Feb-2003  
           TrEMBL\_new of 07-Feb-2003

### List of potentially matching sequences

Send selected sequences to [Clustal W \(multiple alignment\)](#)

☐ Include query sequence

| Db AC  | Description  | Score               | E-value |
|--|--|---------------------|---------|
| <input type="checkbox"/> tr <a href="#">Q25663</a>   | Serine protease (HTRA) [HP1019] [Helicobacter pylori (...] | <a href="#">834</a> | 0.0     |
| <input type="checkbox"/> tr <a href="#">Q9ZM18</a>   | Protease DO [HTRA] [Helicobacter pylori J99 (Campyloba...  | <a href="#">813</a> | 0.0     |
| <input type="checkbox"/> tr <a href="#">Q9PN69</a>   | Serine protease (Protease DO) (EC 3.4.21.-) [HTRA] [Ca...  | <a href="#">388</a> | e-107   |
| <input type="checkbox"/> tr <a href="#">Q46120</a>   | Serine protease [HTRA] [Campylobacter jejuni]              | <a href="#">387</a> | e-106   |
| <input type="checkbox"/> tr <a href="#">Q46094</a>   | Heat shock protein/serine protease (Fragment) [HTRA] [...] | <a href="#">347</a> | 2e-94   |
| <input type="checkbox"/> tr <a href="#">Q8YHL4</a>   | Protease DO (EC 3.4.21.-) [BMEI0783] [Brucella meliten...  | <a href="#">291</a> | 1e-77   |
| <input type="checkbox"/> tn <a href="#">AAN30126</a> | Serine protease [BR1207] [Brucella suis]                   | <a href="#">291</a> | 1e-77   |

|                          |    |                          |  |                     |       |
|--------------------------|----|--------------------------|--|---------------------|-------|
| <input type="checkbox"/> | tr | <a href="#">Q44596</a>   | HtrA-like protein [Brucella abortus]                       | <a href="#">289</a> | 4e-77 |
| <input type="checkbox"/> | sp | <a href="#">P18584</a>   | DEGP_CHLTR Probable serine protease do-like precursor ...  | <a href="#">289</a> | 5e-77 |
| <input type="checkbox"/> | tr | <a href="#">Q9FD11</a>   | HtrA-like serine protease [PRTS1] [Aeromonas hydrophila]   | <a href="#">288</a> | 7e-77 |
| <input type="checkbox"/> | tn | <a href="#">AAN56917</a> | Serine protease, HtrA/DegQ/DegS family [SO3942] [She...]   | <a href="#">287</a> | 2e-76 |
| <input type="checkbox"/> | tr | <a href="#">Q9KUF5</a>   | Protease DO [VC0566] [Vibrio cholerae]                     | <a href="#">286</a> | 3e-76 |
| <input type="checkbox"/> | tr | <a href="#">Q8XV99</a>   | Probable HTRA-like serine protease signal peptide prot...  | <a href="#">286</a> | 3e-76 |
| <input type="checkbox"/> | tn | <a href="#">AAO09118</a> | Protease DO [VV10603] [Vibrio vulnificus]                  | <a href="#">286</a> | 3e-76 |
| <input type="checkbox"/> | sp | <a href="#">Q9PL97</a>   | DEGP_CHLMU Probable serine protease do-like precursor ...  | <a href="#">285</a> | 6e-76 |
| <input type="checkbox"/> | tr | <a href="#">Q8KCH4</a>   | Serine protease [CT1447] [Chlorobium tepidum]              | <a href="#">285</a> | 6e-76 |
| <input type="checkbox"/> | sp | <a href="#">Q9Z6T0</a>   | DEGP_CHLPN Probable serine protease do-like precursor ...  | <a href="#">282</a> | 5e-75 |
| <input type="checkbox"/> | tr | <a href="#">Q8L1C3</a>   | DegQ serine protease [Pasteurella piscicida (Photobact...] | <a href="#">276</a> | 4e-73 |
| <input type="checkbox"/> | tn | <a href="#">BAC24289</a> | DegQ protein [degQ] [Wigglesworthia brevipalpis]           | <a href="#">276</a> | 5e-73 |
| <input type="checkbox"/> | tn | <a href="#">AAN66925</a> | HtrA-like protease AlgW [algW] [Pseudomonas putida]        | <a href="#">275</a> | 1e-72 |
| <input type="checkbox"/> | tr | <a href="#">Q57155</a>   | MUCD (Serine protease MUCD) [MUCD] [Pseudomonas aerugi...] | <a href="#">273</a> | 2e-72 |
| <input type="checkbox"/> | tr | <a href="#">Q9ALS1</a>   | MucD [MUCD] [Pseudomonas aeruginosa]                       | <a href="#">273</a> | 2e-72 |
| <input type="checkbox"/> | tr | <a href="#">Q8Z9B0</a>   | Protease DO, heat shock protein HtrA [STY0231] [Salmon...] | <a href="#">272</a> | 5e-72 |
| <input type="checkbox"/> | tn | <a href="#">AAN78691</a> | Protease do precursor (EC 3.4.21.-) [htrA] [Escheric...]   | <a href="#">272</a> | 7e-72 |
| <input type="checkbox"/> | sp | <a href="#">P26982</a>   | DEGP_SALTY Protease do precursor (EC 3.4.21.-) [DEGP] ...  | <a href="#">271</a> | 1e-71 |
| <input type="checkbox"/> | tn | <a href="#">BAC50633</a> | Serine protease [bll5368] [Bradyrhizobium japonicum]       | <a href="#">271</a> | 2e-71 |
| <input type="checkbox"/> | sp | <a href="#">P09376</a>   | DEGP_ECOLI Protease do precursor (EC 3.4.21.-) [DEGP] ...  | <a href="#">270</a> | 2e-71 |
| <input type="checkbox"/> | tn | <a href="#">AAN41816</a> | Periplasmic serine protease Do, heat shock protein H...    | <a href="#">268</a> | 1e-70 |
| <input type="checkbox"/> | tr | <a href="#">Q98CS8</a>   | Serine protease, HtrA/DegQ/DegS family [MLL5022] [Rhiz...] | <a href="#">267</a> | 2e-70 |
| <input type="checkbox"/> | tr | <a href="#">O67436</a>   | Periplasmic serine protease [HTRA] [Aquifex aeolicus]      | <a href="#">264</a> | 1e-69 |
| <input type="checkbox"/> | tr | <a href="#">Q9LBK0</a>   | Heat shock protein HtrA [HTRA] [Shigella sonnei]           | <a href="#">264</a> | 1e-69 |
| <input type="checkbox"/> | tr | <a href="#">Q9HVX1</a>   | AlgW protein [ALGW] [Pseudomonas aeruginosa]               | <a href="#">263</a> | 2e-69 |
| <input type="checkbox"/> | sp | <a href="#">P45129</a>   | HTOA_HAEIN Probable periplasmic serine protease do/hho...  | <a href="#">262</a> | 5e-69 |
| <input type="checkbox"/> | tr | <a href="#">Q8RSS1</a>   | HtrA protein [HTRA] [Klebsiella pneumoniae]                | <a href="#">262</a> | 5e-69 |
| <input type="checkbox"/> | tr | <a href="#">Q8ZB58</a>   | Protease (EC 3.4.21.-) [DEGQ] [Yersinia pestis]            | <a href="#">262</a> | 7e-69 |
| <input type="checkbox"/> | tn | <a href="#">AAM83731</a> | Serine endoprotease [degQ] [Yersinia pestis]               | <a href="#">262</a> | 7e-69 |
| <input type="checkbox"/> | tr | <a href="#">Q9AQD1</a>   | MucD [MUCD] [Pseudomonas syringae (pv. syringae)]          | <a href="#">260</a> | 3e-68 |
| <input type="checkbox"/> | tr | <a href="#">Q8UE46</a>   | Serine protease [HTRA] [Agrobacterium tumefaciens (str...] | <a href="#">259</a> | 6e-68 |
| <input type="checkbox"/> | tr | <a href="#">Q8UGQ8</a>   | Serine protease DO-like protease [DOP] [Agrobacterium ...] | <a href="#">258</a> | 8e-68 |
| <input type="checkbox"/> | tr | <a href="#">O68198</a>   | HtrA [Haemophilus influenzae]                              | <a href="#">257</a> | 2e-67 |
| <input type="checkbox"/> | tr | <a href="#">O68197</a>   | HtrA (Fragment) [Haemophilus influenzae]                   | <a href="#">257</a> | 2e-67 |
| <input type="checkbox"/> | tr | <a href="#">O31388</a>   | DegP protein [DEGP] [Bradyrhizobium japonicum]             | <a href="#">256</a> | 3e-67 |
| <input type="checkbox"/> | tn | <a href="#">BAC50500</a> | Serine protease [degP] [Bradyrhizobium japonicum]          | <a href="#">256</a> | 3e-67 |
| <input type="checkbox"/> | sp | <a href="#">Q92JA1</a>   | DEGP_RICCN Probable serine protease do-like precursor ...  | <a href="#">255</a> | 7e-67 |
| <input type="checkbox"/> | tn | <a href="#">AAN67052</a> | Alginate biosynthesis negative regulator, serine pro...    | <a href="#">255</a> | 7e-67 |
| <input type="checkbox"/> | tr | <a href="#">Q8P418</a>   | Protease Do [HTRA] [Xanthomonas campestris (pv. campes...] | <a href="#">254</a> | 1e-66 |
| <input type="checkbox"/> | tr | <a href="#">Q9CMS7</a>   | HtrA [HTRA] [Pasteurella multocida]                        | <a href="#">254</a> | 1e-66 |
| <input type="checkbox"/> | tr | <a href="#">P74978</a>   | GsrA protein [GSRA] [Yersinia enterocolitica]              | <a href="#">254</a> | 1e-66 |
| <input type="checkbox"/> | sp | <a href="#">P39099</a>   | DEGQ_ECOLI Protease degQ precursor (EC 3.4.21.-) [DEGQ...] | <a href="#">253</a> | 2e-66 |
| <input type="checkbox"/> | tr | <a href="#">Q8X9F1</a>   | Serine endoprotease [DEGQ] [Escherichia coli O157:H7]      | <a href="#">253</a> | 2e-66 |
| <input type="checkbox"/> | tr | <a href="#">Q8ZBM6</a>   | Global stress requirement protein GsrA [GSRA] [Yersini...] | <a href="#">253</a> | 2e-66 |
| <input type="checkbox"/> | tn | <a href="#">AAM84394</a> | Periplasmic serine protease Do [htrA] [Yersinia pestis]    | <a href="#">253</a> | 2e-66 |

|                          |    |                          |   |                     |       |
|--------------------------|----|--------------------------|---|---------------------|-------|
| <input type="checkbox"/> | tn | <a href="#">AAN82429</a> | Protease degQ precursor (EC 3.4.21.-) [degQ] [Escher...   | <a href="#">253</a> | 2e-66 |
| <input type="checkbox"/> | sp | <a href="#">Q44597</a>   | DEGP_BRUAB Probable serine protease do-like precursor ... | <a href="#">252</a> | 6e-66 |
| <input type="checkbox"/> | tr | <a href="#">Q8PFK1</a>   | Protease DO [HTRA] [Xanthomonas axonopodis (pv. citri)]   | <a href="#">252</a> | 6e-66 |
| <input type="checkbox"/> | tr | <a href="#">Q8YG32</a>   | Protease DO (EC 3.4.21.-) [BMEI1330] [Brucella meliten... | <a href="#">252</a> | 6e-66 |
| <input type="checkbox"/> | tn | <a href="#">BAC48395</a> | Serine protease DO-like precursor [blr3130] [Bradyrh...   | <a href="#">252</a> | 7e-66 |
| <input type="checkbox"/> | sp | <a href="#">P57322</a>   | DEGP_BUCAI Probable serine protease do-like precursor ... | <a href="#">251</a> | 1e-65 |
| <input type="checkbox"/> | tr | <a href="#">Q8UDS7</a>   | Serine protease DO-like [HTRA] [Agrobacterium tumefaci... | <a href="#">251</a> | 1e-65 |
| <input type="checkbox"/> | tn | <a href="#">AAO26942</a> | Serine protease (EC 3.4.21.-) [htrA] [Buchnera aphid...   | <a href="#">251</a> | 2e-65 |
| <input type="checkbox"/> | tr | <a href="#">Q8Z3E6</a>   | Serine protease (EC 3.4.21.-) [DEGQ] [Salmonella typhi]   | <a href="#">248</a> | 8e-65 |
| <input type="checkbox"/> | tr | <a href="#">Q98N31</a>   | Heat shock protein HtrA like [MLR0328] [Rhizobium loti... | <a href="#">247</a> | 2e-64 |
| <input type="checkbox"/> | tr | <a href="#">Q8ZLQ1</a>   | Serine endoprotease (EC 3.4.21.-) [DEGQ] [Salmonella t... | <a href="#">247</a> | 2e-64 |
| <input type="checkbox"/> | tr | <a href="#">Q9PGL3</a>   | Heat shock protein [XF0285] [Xylella fastidiosa]          | <a href="#">247</a> | 2e-64 |
| <input type="checkbox"/> | tr | <a href="#">Q8KKV0</a>   | Hypothetical protein [HTRA] [Rhizobium etli]              | <a href="#">247</a> | 2e-64 |
| <input type="checkbox"/> | tn | <a href="#">AAO28122</a> | Heat shock protein [htrA] [Xylella fastidiosa Temecu...   | <a href="#">247</a> | 2e-64 |
| <input type="checkbox"/> | tr | <a href="#">Q8XPT5</a>   | Probable protease signal peptide protein (EC 3.4.-.-) ... | <a href="#">246</a> | 5e-64 |
| <input type="checkbox"/> | sp | <a href="#">O85291</a>   | DEGP_BUCAP Probable serine protease do-like precursor ... | <a href="#">245</a> | 7e-64 |
| <input type="checkbox"/> | tn | <a href="#">BAC51771</a> | Serine protease DO-like precursor [bll6506] [Bradyrh...   | <a href="#">245</a> | 7e-64 |
| <input type="checkbox"/> | tr | <a href="#">Q985F9</a>   | Serine protease [MLR7692] [Rhizobium loti (Mesorhizobi... | <a href="#">244</a> | 2e-63 |
| <input type="checkbox"/> | tr | <a href="#">Q56885</a>   | HtrA protein (Fragment) [HTRA] [Yersinia enterocolitica]  | <a href="#">244</a> | 2e-63 |
| <input type="checkbox"/> | tn | <a href="#">BAC47856</a> | Serine protease DO-like protease [dop] [Bradyrhizobi...   | <a href="#">244</a> | 2e-63 |
| <input type="checkbox"/> | tr | <a href="#">Q92QE6</a>   | Probable protease protein (EC 3.4.21.-) [DEGP3] [Rhizo... | <a href="#">243</a> | 3e-63 |
| <input type="checkbox"/> | tr | <a href="#">Q44652</a>   | Immunoreactive stress response protein precursor [Bruc... | <a href="#">240</a> | 3e-62 |
| <input type="checkbox"/> | tr | <a href="#">Q98KJ1</a>   | Probable serine protease [MLL1451] [Rhizobium loti (Me... | <a href="#">239</a> | 5e-62 |
| <input type="checkbox"/> | tr | <a href="#">Q9PBA3</a>   | Periplasmic protease [XF2241] [Xylella fastidiosa]        | <a href="#">238</a> | 8e-62 |
| <input type="checkbox"/> | tn | <a href="#">AAO29135</a> | Periplasmic protease [mucD] [Xylella fastidiosa Teme...   | <a href="#">237</a> | 2e-61 |
| <input type="checkbox"/> | tr | <a href="#">Q926C8</a>   | Putative protease precursor signal peptide protein (EC... | <a href="#">237</a> | 2e-61 |
| <input type="checkbox"/> | tr | <a href="#">Q8PB56</a>   | Periplasmic protease [MUCD] [Xanthomonas campestris (p... | <a href="#">234</a> | 1e-60 |
| <input type="checkbox"/> | tr | <a href="#">Q8PMV4</a>   | Periplasmic protease [MUCD] [Xanthomonas axonopodis (p... | <a href="#">234</a> | 1e-60 |
| <input type="checkbox"/> | tr | <a href="#">Q8RTK2</a>   | Protease MucD [MUCD] [Xanthomonas campestris (pv. camp... | <a href="#">234</a> | 1e-60 |
| <input type="checkbox"/> | tn | <a href="#">AAN44738</a> | Serine endoprotease [degQ] [Shigella flexneri]            | <a href="#">234</a> | 1e-60 |
| <input type="checkbox"/> | sp | <a href="#">O05942</a>   | DEGP_RICPR Probable serine protease do-like precursor ... | <a href="#">234</a> | 2e-60 |
| <input type="checkbox"/> | sp | <a href="#">P54925</a>   | DEGP_BARHE Probable periplasmic serine protease DO-lik... | <a href="#">233</a> | 3e-60 |
| <input type="checkbox"/> | sp | <a href="#">Q52894</a>   | DEGP_RHIME Probable serine protease do-like precursor ... | <a href="#">232</a> | 6e-60 |
| <input type="checkbox"/> | tr | <a href="#">Q8Y0I6</a>   | Probable periplasmic protease signal peptide protein (... | <a href="#">231</a> | 1e-59 |
| <input type="checkbox"/> | tr | <a href="#">P73354</a>   | Serine protease HTRA [HTRA] [Synechocystis sp. (strain... | <a href="#">231</a> | 1e-59 |
| <input type="checkbox"/> | tr | <a href="#">Q9JVT1</a>   | Putative periplasmic serine protease (EC 3.4.21.-) [NM... | <a href="#">230</a> | 3e-59 |
| <input type="checkbox"/> | tn | <a href="#">AAN48008</a> | Serine protease DO [LA0809] [Leptospira interrogans]      | <a href="#">229</a> | 4e-59 |
| <input type="checkbox"/> | tr | <a href="#">Q8YI32</a>   | Protease DO (EC 3.4.21.-) [BMEI0613] [Brucella meliten... | <a href="#">228</a> | 9e-59 |
| <input type="checkbox"/> | tn | <a href="#">AAN30307</a> | Serine protease Do, putative [BR1394] [Brucella suis]     | <a href="#">228</a> | 9e-59 |
| <input type="checkbox"/> | tr | <a href="#">Q9KJN6</a>   | Putative serine protease DO-like [HTRA] [Myxococcus xa... | <a href="#">225</a> | 1e-57 |
| <input type="checkbox"/> | tr | <a href="#">Q9A4S2</a>   | Serine protease HtrA [CC2758] [Caulobacter crescentus]    | <a href="#">223</a> | 4e-57 |
| <input type="checkbox"/> | tr | <a href="#">O06439</a>   | ORF E0 protein [Rhodobacter capsulatus (Rhodopseudomon... | <a href="#">222</a> | 8e-57 |
| <input type="checkbox"/> | tn | <a href="#">BAC08222</a> | Periplasmic serine proteinase [tlr0671] [Synechococc...   | <a href="#">219</a> | 7e-56 |
| <input type="checkbox"/> | tr | <a href="#">Q9WZ41</a>   | Heat shock serine protease, periplasmic [TM0571] [Ther... | <a href="#">218</a> | 9e-56 |
| <input type="checkbox"/> | tr | <a href="#">Q51374</a>   | AlgW [Pseudomonas aeruginosa]                             | <a href="#">218</a> | 1e-55 |

|                          |           |   |     |       |
|--------------------------|-----------|---|-----|-------|
| <input type="checkbox"/> | tr Q8YVH0 | Serine proteinase [ALL2008] [Anabaena sp. (strain PCC ... | 215 | 1e-54 |
| <input type="checkbox"/> | sp P44947 | DEGS_HAEIN Protease degS precursor (EC 3.4.21.-) [DEGS... | 214 | 2e-54 |
| <input type="checkbox"/> | tr Q9A8R9 | Serine protease [CC1282] [Caulobacter crescentus]         | 209 | 7e-53 |

## Graphical overview of the alignments

[Click here](#)to resubmit your query after masking regions matching [PROSITE](#) profiles or [Pfam](#) HMMs

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(use [ScanProsite](#) for more details about PROSITE matches)

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Alignments



tr 025663 Serine protease (HTRA) [HP1019] [Helicobacter pylori] 443 AA  
(Campylobacter align  
pylori)]

Score = 834 bits (2154), Expect = 0.0  
Identities = 430/443 (97%), Positives = 430/443 (97%)

Query: 1 MSPLKTIRIYSYHDSIKDSIKAVVNISTEKKIKNNFIGGGVFNDPFFQQFFGDLGGMIPK 60  
MSPLKTIRIYSYHDSIKDSIKAVVNISTEKKIKNNFIGGGVFNDPFFQQFFGDLGGMIPK  
Sbjct: 1 MSPLKTIRIYSYHDSIKDSIKAVVNISTEKKIKNNFIGGGVFNDPFFQQFFGDLGGMIPK 60

Query: 61 ERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIR 120  
ERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIR  
Sbjct: 61 ERMERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIR 120

Query: 121 ITKDNLPITIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQT 180  
ITKDNLPITIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQT  
Sbjct: 121 ITKDNLPITIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQT 180

Query: 181 DASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDVTVTQLIKTGKIE 240  
DASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDVTVTQLIKTGKIE  
Sbjct: 181 DASINPGNSGGALIDSRGGLVGINTAIISKTGGNHGIGFAIPSNMVKDVTVTQLIKTGKIE 240

Query: 241 RGYLGVLQDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNE 300  
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Sbjct: 241 RGYLGVLQDLQNSYDNKEGAVVISVEKDSPAKKAGILVWDLITEVNGKKVKNTNE 300

Query: 301 LRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISXXXXXXXXXXXXXVED 360  
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Sbjct: 301 LRNLIGSMLPNQRVTLKVIRDKKERAFTLTLAERKNPNKKETISAQNGAQQQLNGLQVED 360

Query: 361 LTQETKRSMRLSDDVQGVVLSQVNENSPAEQAGFRQGNIIITKIEEVEVKSVADFNHALEK 420  
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Sbjct: 361 LTQETKRSMRLSDDVQGVVLSQVNENSPAEQAGFRQGNIIITKIEEVEVKSVADFNHALEK 420

Query: 421 YKGKPKRFLVLDLNQGYRIILVK 443  
YKGKPKRFLVLDLNQGYRIILVK  
Sbjct: 421 YKGKPKRFLVLDLNQGYRIILVK 443

tr Q9ZM18 **Protease DO [HTRA] [Helicobacter pylori J99 (Campylobacter pylori J99)]** 476 AA  
align

Score = 813 bits (2099), Expect = 0.0  
Identities = 420/441 (95%), Positives = 421/441 (95%)

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P K IYSYHDSIKDSIKAVVNISTEKKIKNNFIGGGVFNDPFFQQFFGDLGGMIPKER  
Sbjct: 36 PSKEDTIYSYHDSIKDSIKAVVNISTEKKIKNNFIGGGVFNDPFFQQFFGDLGGMIPKER 95

Query: 63 MERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRIT 122  
MERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRIT  
Sbjct: 96 MERALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSESDLAVIRIT 155

Query: 123 KDNLPITIKFSDSNDISVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDA 182  
KDNLPITIKFSDSNDI VGDVLFVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDA  
Sbjct: 156 KDNLPITIKFSDSNDILVGDLVFAIGNPFGVGESVTQGIVSALNKSGIGINSYENFIQTDA 215

Query: 183 SINPGNSGGALIDSRGGLVGINTAIISKTTGGNHGIGFAIPSNMVKDVTQLIKTGKIERG 242  
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Sbjct: 216 SINPGNSGGALIDSRGGLVGINTAIISKTTGGNHGIGFAIPSNMVKDIVTQLIKTGKIERG 275

Query: 243 YLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAAGILVWDLITEVNGKKVKNTNELR 302  
YLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAAGILVWDLITEVNGKKVKNTNELR  
Sbjct: 276 YLGVGLQDLSGDLQNSYDNKEGAVVISVEKDSPAAGILVWDLITEVNGKKVKNTNELR 335

Query: 303 NLIGSMLPNQRVTLKVIRDKKERAFVTLTLAERKNPNKKETISXXXXXXXXXXXXVEDLT 362  
NLIGSMLPNQRVTLKVIRDKKER FTLTLAERKNPNKKETIS VEDLT  
Sbjct: 336 NLIGSMLPNQRVTLKVIRDKKERTFTLTLAERKNPNKKETISAQNGVQGQLNGLQVEDLT 395

Query: 363 QETKRSMRLSDDVQGVVLSQVNENSPAEGAGFRQGNIIITKIEEVEVKSVADFNHALEKYK 422  
Q+TKRSMRLSDDVQGVVLSQVNENSPAEGAGFRQGNIIITKIEEVEVKSVADFNHALEKYK  
Sbjct: 396 QETKRSMRLSDDVQGVVLSQVNENSPAEGAGFRQGNIIITKIEEVEVKSVADFNHALEKYK 455

Query: 423 GKPKRFLVLDLNQGYRIILVK 443  
GKPKRFLVLDLNQGYRIILVK  
Sbjct: 456 GKPKRFLVLDLNQGYRIILVK 476

tr Q9PN69 **Serine protease (Protease DO) (EC 3.4.21.-) [HTRA]** 472 AA  
[Campylobacter  
jejuni] align

Score = 388 bits (996), Expect = e-107

Identities = 212/431 (49%), Positives = 291/431 (67%), Gaps = 15/431 (3%)

Query: 1 MSPLKTIRIYSYHDSIKDSIKAVVNISTEKKIKNNFIGGGV---FNDPFFQQFFG-DLGG 56  
++P + SYHDSIKD+ K+VVNIST K I + FNDP+F+QFF D  
Sbjct: 31 VNPAAGNAVLSYHDSIKDAKKS VVNISTSKTITRANRPSPLDDFFNDPYFKQFFDFDFSQ 90

Query: 57 MIPKERME--RALGSGVIISKDGYIVTNNHVIDGADKIKVTIPGSNKEYSATLVGTDSES 114  
K E +LGSGVIISKDGYIVTNNHV+D AD I V +PGS+ EY A L+G D ++  
Sbjct: 91 RKGKNDKEVVSSLGSGVIISKDGYIVTNNHVDDADTITVNLPGSDIEYKAKLIGKDPKT 150

Query: 115 DLAVIRITKDNLPITIKFSDSNDISVGD LVFAIGNPFGVGESVTQGIVSALNKSGIGINSY 174  
DLAVI+I +NL I F++S+D+ GD+VFA+GNPFGVG SVT GI+SALNK IG+N Y  
Sbjct: 151 DLAVIKIEANNLSAITFTNSDDLMEGDVVFALGNPFGVGSVTSGIISALNKDNI GLNQY 210

Query: 175 ENFIQT DASINPGNSGGALIDSRGGLVGINTAIISK TGGNHGIGFAIPSNMVKDTVTQLI 234  
ENFIQT DASINPGNSGGAL+DSRG LVGIN+AI+S+ GGN+GIGFAIPSNMVKD +LI  
Sbjct: 211 ENFIQT DASINPGNSGGALVDSRGYLVGINSAILSRGGGNGIGFAIPSNMVKDIAKKLI 270

Query: 235 KTGKIERGYLGVLQDL SGLQNSYDNKEGAVVISVEKDS PAKKAGILVWDLITEVNGKK 294  
+ GKI+RG+LGV + L GD + +Y N+EGA++ V+K S A +AG+ DL+T+VN K  
Sbjct: 271 EKGKIDRGFLGV TILALQGD TTKAYKNQEGALITDVQKGSSADEAGLKRGD LVTKVNDKV 330

Query: 295 VKNTNELRNLI G SMLPNQRVTLKVIRD-KKERAFTLT LAERKNPNK KETISXXXXXXXXXX 353  
+K+ +L+N IG++ Q+++L RD + ++A + E++NP ++  
Sbjct: 331 IKSPIDLKNYIGTLEIGQKISLSYERDGENKQASFILKGEKENPKGVQS-----DLI 382

Query: 354 XXXXVEDLTQETKRSMRLSDDVQGV LVSQVNENSPA EQAGFRQGNII TKIEEVEVKSVAD 413  
+ +L K +++ DV GVLV V E S + +GF++G+II + + E+K++ D  
Sbjct: 383 DGLSLRNLD PRLKDR LQIPKDVNGVLVDSVKEKSKGKNSGFQEGDIIIGVGQSEIKNLKD 442

Query: 414 FNHALEKYKGK 424  
AL++ K  
Sbjct: 443 LEQALKQVNKK 453

SYSTEM:OS - DIALOG OneSearch

File 155:MEDLINE(R) 1966-2003/Feb W2

(c) format only 2003 The Dialog Corp.

File 349:PCT FULLTEXT 1979-2002/UB=20030206,20030123

(c) 2003 WIPO/Univentio

File 5:Biosis Previews(R) 1969-2003/Feb W2

(c) 2003 BIOSIS

\*File 5: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 449:IMS Company Profiles 1992-2003/Mar

(c) 2003 IMS Health & Affiliates

File 34:SciSearch(R) Cited Ref Sci 1990-2003/Feb W2

(c) 2003 Inst for Sci Info

\*File 34: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 71:ELSEVIER BIOBASE 1994-2003/Feb W2

(c) 2003 Elsevier Science B.V.

File 73:EMBASE 1974-2003/Feb W1

(c) 2003 Elsevier Science B.V.

\*File 73: Alert feature enhanced for multiple files, duplicates removal, customized scheduling. See HELP ALERT.

File 440:Current Contents Search(R) 1990-2003/Feb 13

(c) 2003 Inst for Sci Info

\*File 440: Daily alerts are now available.

File 65:Inside Conferences 1993-2003/Feb W2

(c) 2003 BLDSC all rts. reserv.

File 636:Gale Group Newsletter DB(TM) 1987-2003/Feb 12

(c) 2003 The Gale Group

File 144:Pascal 1973-2003/Feb W1

(c) 2003 INIST/CNRS

File 399:CA SEARCH(R) 1967-2003/UD=13807

(c) 2003 American Chemical Society

\*File 399: Use is subject to the terms of your user/customer agreement.  
Alert feature enhanced for multiple files, etc. See HELP ALERT.

Set Items Description

--- ----

Cost is in DialUnits

?ds

Set Items Description

S1 25 HTRA (10N) (PYLROI OR PYLORI OR PYLORIS OR PYLORIDIS OR PY-  
LORUM OR HPYLORI? OR HELICOBACTER?)

S2 15 RD (unique items)

?t s2/9/13

2/9/13 (Item 1 from file: 65)

DIALOG(R)File 65:Inside Conferences

(c) 2003 BLDSC all rts. reserv. All rts. reserv.

00453860 INSIDE CONFERENCE ITEM ID: CN004355891

**Molecular Cloning and Nucleotide Sequence Determination of htrA , a Gene  
Encoding a 48-kDa Stress Protein of Helicobacter pylori**

Kleanthous, H.; Clayton, C. L.; Morgan, D. D.; Pallen, M. J.

CONFERENCE: Basic and clinical aspects of helicobacter pylori infection-  
4th Workshop

P: 195-202

New York, Springer-Verlag, c1994

ISBN: 3540567208; 0387567208

LANGUAGE: English DOCUMENT TYPE: Conference Selected papers

CONFERENCE EDITOR(S): Gasbarrini, G.; Pretolani, S.

CONFERENCE SPONSOR: European Helicobacter Pylori Study Group

CONFERENCE LOCATION: Bologna, Italy

CONFERENCE DATE: Nov 1991 (199111) (199111)

BRITISH LIBRARY ITEM LOCATION: 94/09285 Basic

NOTE:

xii, 313 p.; Described as proceedings. See also 4588.3404 vol 23 no 9  
and supp 1 2 1991 for abstracts and programme

DESCRIPTORS: helicobacter pylori infection; helicobacter pylori

?t s2/3,kwic/3-7 9-11

>>>KWIC option is not available in file(s): 399

# WEST Search History

DATE: Thursday, February 13, 2003

## Set Name Query

side by side

## Hit Count Set Name

result set

*DB=USPT; PLUR=YES; OP=AND*

|     |   |     |     |
|-----|---|-----|-----|
| L1  | pox\$.clm.  | 391 | L1  |
| L2  | L1 same (htra or htr-a or proteinase or protease or peptidase)      | 4   | L2  |
| L3  | L1 same (htra or htr-a or proteinase or protease or peptidase).clm. | 4   | L3  |
| L4  | poxv\$.clm.   | 142 | L4  |
| L5  | L4 same (htra or htr-a or proteinase or protease or peptidase).clm. | 1   | L5  |
| L6  | L4 and (htra or htr-a or proteinase or protease or peptidase).clm.  | 2   | L6  |
| L7  | L4 and (serine).clm.  | 1   | L7  |
| L8  | poxv\$ same (htra or htr-a or proteinase or protease or peptidase)  | 40  | L8  |
| L9  | L8 not l3 not l6  | 39  | L9  |
| L10 | L9 same (htr or serine)   | 3   | L10 |
| L11 | L9 same (htra or htr-a or serine)                                   | 3   | L11 |

END OF SEARCH HISTORY